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Leukemia Cancer Cell Detection using Image Processing

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ABSTRACT: The microscopic pictures are examined visually by haematologists and the process is tedious and time taking. The automatic image handling framework is required that can overcome related constraints in visual investigation. The proposed method is effectively connected to a large number of pictures, demonstrating promising results for changing image quality. Distinctive picture handling calculations, for example, Image Enhancement, Clustering, Mathematical morphology and Labelling are executed utilizing MATLAB. Utilizing a portion of the productive image handling instruments, we can identify and section disease cell. The segmentation is used in knowing the exact size and shape of the cancer cell and the area. Initially we have utilized image enhancement strategies to improve the contrast and standardize the pixel values in the picture. Followed by segmentation and at last we apply Feature extraction, after that we have connected it to classifier to get the desired results. The algorithm is been utilized on various pictures of the cancerous cell and has constantly given us the correct desired output.

KEYWORDS: K-mean, GLCM, GLDM, SVM Classifier

I.INTRODUCTION

The most critical part of a human body is blood as it keeps one alive. It performs numerous functions such as, to exchange oxygen, carbon dioxide, and mineral and so on to the entire body with a specific end goal to look after digestion system. Hence any problem in blood such as blood cancer may lead to death in human beings. Blood disease is reparable when it is distinguished and treated at correct time stage. Its acknowledgment starts with a complete blood cloud. If there are abnormalities in this count, an examination of morphological bone marrow smear examination is done to assert the region of carcinogenic cells. In this study, a pathologist watches a couple of cells under a light microscopy hunting down varieties from the standard showed in the center or cytoplasm of the cells in order to portray the strange cells in their particular sorts and subtypes of leukemia. This request is indispensable as it makes sense of which treatment is given. This study has a misstep rate some place around 30% and 40% depending upon the pathologist experience and the inconvenience to perceive leukemia sorts and subtypes. A stream cytometry test is outstandingly exact to organize leukemia's, yet it is greatly expensive and not each one of the mending focuses have the equipment to perform it. The gathering of leukemia sorts and subtypes empower the specialists' work in picking what treatment is the best for a given cell sort (lymphocytic or myelogenous) and disease progress (extraordinary or endless).

This paper shows a pre-processing system for the leukemic cells, remembering the finished objective to make the components well depicting whether the cell is cancerous or not furthermore recognize the sort of leukemia. Leukemia are mainly of four types which are as follows acute lymphocytic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL) and chronic myeloid leukemia (CML). In the pre-processing steps input cell image has to undergo resize the image, color conversion, noise removal, histogram equalization. After pre-processing segmentation is done to the pre-processed image where K-mean clustering algorithm is used. Followed by feature extraction using GLCM and GLDM. Finally SVM classifier is used to classify the cell whether the cell is cancerous or not and also to identify the type of leukemia.

II. RELATED WORK

Diagnostic radiography assigns the technical parts of medical imaging and specifically in acquiring therapeutic images. Dr.s.Venkatachalam [1] presents the pre-processing strategies for the leukemic injected cells image keeping in mind the

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end goal to create the elements well describing different sorts of cells. The tackled issues include: the segmentation of the bone marrow suction by applying the watershed change, determination of individual cells, and texture feature, statistical and geometrical examination of the cells.

Image processing procedures are been generally utilized as a part of medical imaging research. These strategies are valuable for representation, enhancement, segmentation and numerous more operations which are helpful for processing medicinal image which perhaps MRI, CT or whatever other images acquired through one of the imaging methodology. One of the advantages of utilizing these methods is to identify any abnormality from the norm in the image of medical application. Some of these application in detecting tumor, blocked vessels or here and there broken joints. [2] Vinay Parameshwarappa.al proposed a strategy for recognizing one such variation from the norm saw in brain image. Utilizing a portion of the traditional picture handling devices and Fourier transform.

According to Bhagyashri G.Patil [3] overview, as of late Lung growth cell has been gaining the consideration of therapeutic and sciatic groups in the most recent years in light of its high prevalence unified with the difficult treatment. Insights from 2008 demonstrate that lung disease, all through world, is the one that assaults the best number of people. Early identification of lung growth is essential for fruitful treatment. There is couple of strategies accessible to identify dangerous cells. Here two techniques for division, for example, thresholding and watershed are utilized to distinguish the disease cell and too discover better approach out of them.

Fundamental mathematical morphological hypothesis and operations are presented at initially, utilized for identifying the edges and additionally the [4] tumor cells of lungs CT and MRI images. Since, salt and pepper noise are more pervasive in medical images the routine techniques are not successful in sifting salt and pepper noise. [4] Numerical morphological operations are utilized to identify the edges and the disease cells. Morphological disintegration is a decent channel of salt and pepper commotion. The trial results demonstrate that the proposed calculation is more proficient for restorative picture denoising, edge location and recognizable proof than the normally utilized layout based edge identification calculations and general morphological edge recognition algorithm.

III.PROPOSED SYSTEM

Proposed system has two parts training and testing. Both the parts undergo following steps. Image acquisition is the initial step collecting images of the blood from microscope with proper magnification from any of the hospitals. Second step is image preprocessing where following steps are followed initially color conversion takes place, color image is converted to gray scale. Followed by filtering the image, removal of noise from the image and finally histogram equalization is done to improve the quality of image in terms of contrast. Third step is segmentation using k-mean clustering where nucleus is concentrated for the detection process. Segmentation is followed by feature extraction where features of nucleus are extracted using GLCM and GLDM. In the training part features of pure cancer cell is stored in knowledge base. In the testing part, the cell which needs to be tested is taken as input.

And finally SVM classifier with the help of knowledge base is used for classification, where decision is done whether the cell is cancerous or not. If the cell is cancerous then its type is found among acute lymphocytic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL) and chronic myeloid leukemia (CML). Fig. 1 shows the block diagram of proposed system.

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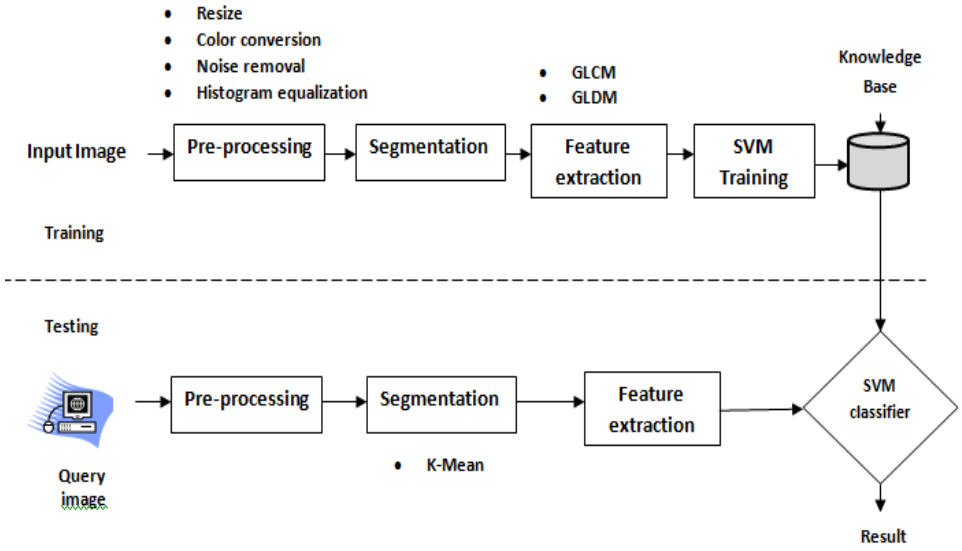

Fig. 1 Architecture of Proposed System

K-MEAN SEGMENTATION: K-Means is a least squares apportioning strategy that partition an accumulation of articles into K groups. K-Means [5] algorithm is an unsupervised grouping algorithm that characterizes the information focuses into different classes in view of their characteristic separation from one another. The algorithms expect that the data features shape a vector space and tries to discover common grouping in them. The main thought is to characterize k centroids, one for every cluster. These centroids ought to be set cunningly as a result of various area causes diverse result. In this way, the better decision is to place them however much as could be expected far from one another. The following step is to take every point having a place with a given data set and partner it to the closest centroid. At the point when no point is pending, the initial step is finished and an early gathering age is finished. As of right now we have to recalculate k new centroids as barycenters of the bunches coming about because of the past step. After we have these k new centroids, another tying must be done between the same information set focuses and the closest new centroid. A circle has been created. As an aftereffect of this circle we might see that the k centroids change their area orderly until no more changes are finished.

The algorithm iterates over following steps:

1. Compute the intensity distribution (also called the histogram) of the intensities.
2. Initialize the centroids with k random intensities.
3. Repeat the following steps until the cluster a label of the image does not change anymore.
4. Cluster the points based on distance of their intensities from the centroid intensities. Equation (1)

$$c(i) = \arg\min_j \|x^{(i)} - \mu_j\| \quad (1)$$

5. Compute the new centroid for each of the clusters.

Where k is a parameter of the algorithm (the number of clusters to be found), i iterates over the all the intensities, j iterates over all the centroids, and μ_j is centroid intensities.

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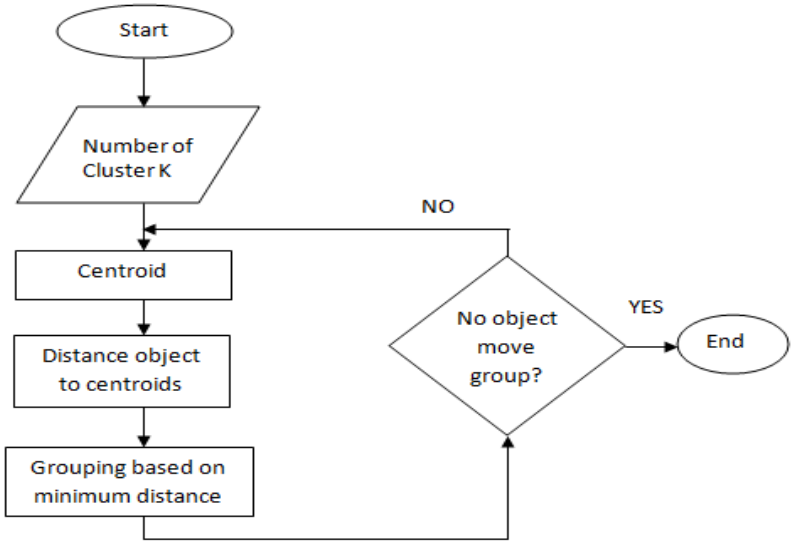

Fig. 2 K-Mean Segmentation

GLDM: The GLDM depends on the event of two pixels which have a given total difference in gray level and which are isolated by a particular displacementδ. For any given displacement vector.

Let S(x, y) = | S(x, y) - S(x+ Δx, y+Δy) and the estimated probability-density function is defined by

$$f(i|\delta)=prob(S\delta(x,y)=i) \quad (2)$$

Use "(2)," to calculate probability-density function.

GLCM: Gray Level Co-Occurrence Matrix (GLCM) has turned out to be a well known factual technique for removing textural highlight from pictures. As per co-event grid, Haralick characterizes fourteen textural highlights measured from the likelihood network to separate the qualities of surface insights of remote detecting pictures. In our proposed system important features like Angular Second Moment (energy), contrast, auto Correlation, Entropy, variance, dissimilarity, homogeneity, cluster prominence and the Inverse Difference Moment are selected for implementation.

SVM CLASSIFIER: SVM is built up as one of standard instruments for machine learning and information mining. This study utilizes the SVM to arrange pictures, which was a factual order framework proposed by Cortes and Vapnik. [6] Uses of an extensive variety of example acknowledgment issues, picture grouping, money related time arrangement expectation, face recognition, biomedical sign investigation, restorative diagnostics, and information mining utilizes SVM now a days. Standard SVM orders objects into two classes by figuring the most extreme edge hyper-plane between the preparation objects of both given classes. Auxiliary danger minimization is connected with such a plan to demonstrate a decent exchange off between low observational danger and little limit.

IV. RESULTS AND DISCUSSION

In the algorithm of nucleus segmentation using matlab the image is enhanced using histogram equalization method (Fig. 4) and nucleus segmentation of enhanced image is done using K mean algorithm. The proposed technique has been applied on microscopic blood slide images. Fig. 3 shows the microscopic input image.

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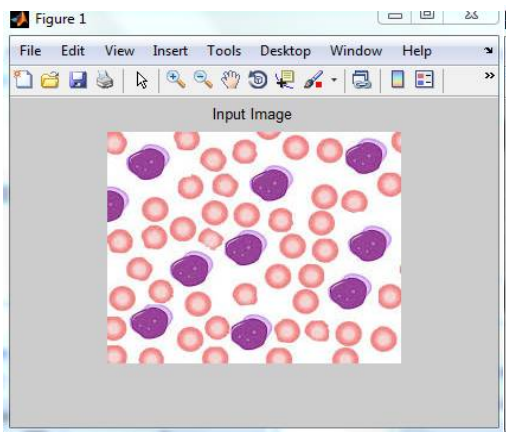

Fig. 3 Input Image

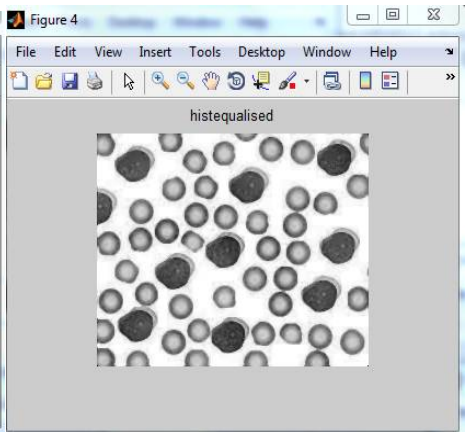

Fig. 4 Enhanced Image

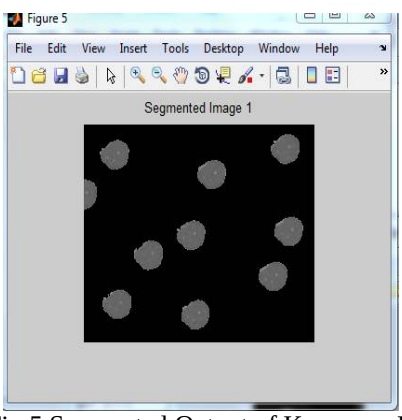

Fig.5 Segmented Output of K-mean

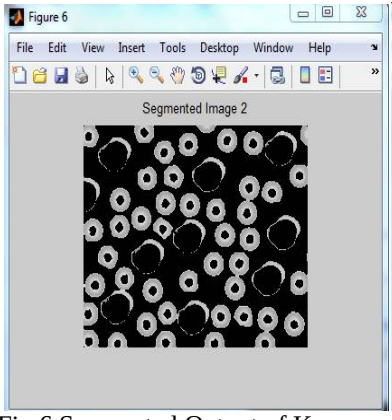

Fig.6 Segmented Output of K-mean

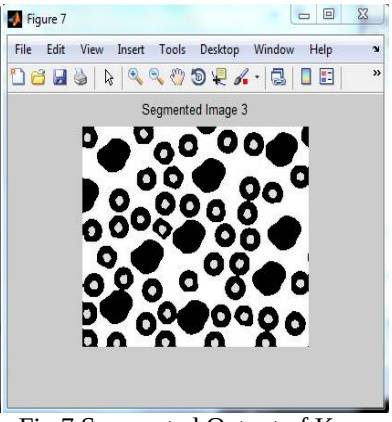

Fig.7 Segmented Output of K-mean

V.CONCLUSION

The main aim of this paper is cell segmentation followed by feature extraction to detect cancer cells. Features of such as Angular Second Moment (energy), contrast, auto Correlation, Entropy, variance, dissimilarity, homogeneity, cluster prominence and the Inverse Difference Moment etc. are considered for better accuracy of detection. The results show that the k mean method is applied for good segmentation performance. In addition, the fully segmented nucleus can be better achieved by using matlab based algorithm because it is less sensitive to input image variations.

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